

SEQUENCE LISTING

<110> University of Iowa Research Foundation et al.

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<120> Novel polypeptides and methods of their use

<130> 875.006W01

10 <150> US 60/105,575

<151> 1998-10-26

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Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile

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Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val

50 55 60

15 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val

65 70 75 80

Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala

85 90 95

Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly

20 100 105 110

Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu

115 120 125

Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe

130 135 140

25 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met

145 150 155 160

Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His

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Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys

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Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His

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Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe

210 215 220

35 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu

225 230 235 240

Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly

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Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe

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 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
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 40 35 40 45

Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
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 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 5 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
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 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
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 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
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 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
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 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 35 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
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 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 40 355 360 365

Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
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 5 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
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 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 30 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 35 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 40 130 135 140

His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 . 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 5 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 10 210 215 220
 Cys Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 15 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 20 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 25 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 30 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 35 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 17
 <211> 449
 <212> PRT
 <213> Artificial Sequence

5

<220>
 <223> A polypeptide encoded by SEQ ID NO:6

<400> 17

10 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Phe Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 15 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 20 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 25 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 30 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 35 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 40 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly

	245	250	255
	Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe		
	260	265	270
	Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg		
5	275	280	285
	Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn		
	290	295	300
	Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp		
	305	310	315
	320		
10	Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met		
	325	330	335
	Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val		
	340	345	350
	Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr		
15	355	360	365
	Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu		
	370	375	380
	Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro		
	385	390	395
	400		
20	Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe		
	405	410	415
	Tyr Arg Ala Tyr Arg Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe		
	420	425	430
	Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp		
25	435	440	445
	Arg		
	<210> 18		
30	<211> 449		
	<212> PRT		
	<213> Artificial Sequence		
	<220>		
35	<223> A polypeptide encoded by SEQ ID NO:7		
	<400> 18		
	Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln		
	1	5	10
	40 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Arg		

	20	25	30
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile			
35	40	45	
Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val			
5 50	55	60	
Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val			
65	70	75	80
Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala			
85	90	95	
10 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly			
100	105	110	
Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu			
115	120	125	
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe			
15 130	135	140	
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met			
145	150	155	160
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His			
165	170	175	
20 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys			
180	185	190	
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His			
195	200	205	
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe			
25 210	215	220	
Ala Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu			
225	230	235	240
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly			
245	250	255	
30 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe			
260	265	270	
Gly Gly Ser Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg			
275	280	285	
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn			
35 290	295	300	
Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp			
305	310	315	320
Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met			
325	330	335	
40 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val			

145	150	155	160
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His			
165	170	175	
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys			
5	180	185	190
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His			
195	200	205	
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe			
210	215	220	
10	Cys Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu		
225	230	235	240
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly			
245	250	255	
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe			
15	260	265	270
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg			
275	280	285	
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn			
290	295	300	
20	Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp		
305	310	315	320
Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met			
325	330	335	
Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val			
25	340	345	350
Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr			
355	360	365	
Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu			
370	375	380	
30	Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro		
385	390	395	400
Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe			
405	410	415	
Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe			
35	420	425	430
Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp			
435	440	445	
Arg			

	85	90	95													
Lys	Gly	Phe	Val	Cys	Ser	Tyr	His	Gly	Trp	Gly	Phe	Gly	Ser	Asn	Gly	
		100						105							110	
Glu	Leu	Gln	Ser	Val	Pro	Phe	Glu	Lys	Glu	Leu	Tyr	Gly	Glu	Ser	Leu	
		5		115			120								125	
Asn	Lys	Lys	Cys	Leu	Gly	Leu	Lys	Glu	Val	Ala	Arg	Val	Glu	Ser	Phe	
				130			135								140	
His	Gly	Phe	Ile	Tyr	Gly	Cys	Phe	Asp	Gln	Glu	Ala	Pro	Ser	Leu	Met	
				145			150			155					160	
10	Asp	Tyr	Leu	Gly	Asp	Ala	Ala	Trp	Tyr	Leu	Glu	Pro	Ile	Phe	Lys	His
				165			170								175	
Ser	Gly	Gly	Leu	Glu	Leu	Val	Gly	Pro	Pro	Gly	Lys	Val	Val	Ile	Lys	
				180			185								190	
Ala	Asn	Trp	Lys	Ala	Pro	Ala	Glu	Asn	Phe	Val	Gly	Asp	Ala	Tyr	His	
				195			200								205	
Val	Gly	Trp	Thr	His	Ala	Ser	Ser	Leu	Arg	Thr	Gly	Glu	Ser	Ile	Phe	
				210			215								220	
Ser	Ser	Leu	Ala	Gly	Asn	Ala	Val	Leu	Pro	Pro	Glu	Gly	Ala	Gly	Leu	
				225			230			235					240	
20	Gln	Met	Thr	Ser	Lys	Tyr	Gly	Ser	Gly	Met	Gly	Val	Leu	Trp	Asp	Gly
				245			250								255	
Tyr	Ser	Gly	Val	His	Ser	Ala	Asp	Leu	Val	Pro	Glu	Leu	Met	Ala	Phe	
				260			265								270	
Gly	Gly	Ala	Lys	Gln	Glu	Arg	Leu	Asn	Lys	Glu	Ile	Gly	Asp	Val	Pro	
				275			280								285	
25	Ala	Arg	Ile	Tyr	Arg	Ser	His	Leu	Asn	Cys	Thr	Val	Phe	Pro	Asn	Asn
				290			295								300	
Ser	Val	Leu	Thr	Cys	Ser	Gly	Val	Phe	Lys	Val	Trp	Asn	Pro	Ile	Asp	
				305			310			315					320	
30	Ala	Asn	Thr	Thr	Glu	Val	Trp	Thr	Tyr	Ala	Ile	Val	Glu	Lys	Asp	Met
				325			330								335	
Pro	Glu	Asp	Leu	Lys	Arg	Arg	Leu	Ala	Asp	Ala	Val	Gln	Arg	Thr	Val	
				340			345								350	
Gly	Pro	Ala	Gly	Phe	Trp	Glu	Ser	Asp	Asp	Asn	Asp	Asn	Asn	Met	Glu	Thr
				355			360								365	
35	Ala	Ser	Gln	Asn	Gly	Lys	Tyr	Gln	Ser	Arg	Asp	Ser	Asp	Leu	Ile	
				370			375								380	
Ser	Asn	Leu	Gly	Phe	Gly	Lys	Asp	Val	Tyr	Gly	Asp	Ala	Val	Tyr	Pro	
				385			390			395					400	
40	Gly	Val	Val	Gly	Lys	Ser	Ala	Ile	Gly	Glu	Thr	Ser	Tyr	Arg	Phe	

	405	410	415
	Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe		
	420	425	430
	Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp		
5	435	440	445
	Arg		

	<210> 20		
10	<211> 449		
	<212> PRT		
	<213> Artificial Sequence		
	<220>		
15	<223> A polypeptide encoded by SEQ ID NO:9		
	<400> 20		
	Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln		
1	5	10	15
20	Lys His Leu Ile His Gly Gly Glu Gly Leu Phe Gln His Glu Leu Arg		
	25	30	
	Ala Val Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile		
	35	40	45
	Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val		
25	50	55	60
	Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val		
65	70	75	80
	Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala		
	85	90	95
30	Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly		
	100	105	110
	Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu		
	115	120	125
	Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe		
35	130	135	140
	His Gly Phe Ile Tyr Ala Cys Ile Asp Gln Glu Ala Pro Ser Leu Met		
145	150	155	160
	Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His		
	165	170	175
40	Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys		

	180	185	190
	Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His		
195	200	205	
	Val Gly Trp Thr His Ala Ser Ser Leu Cys Thr Gly Glu Ser Ile Phe		
5	210	215	220
	Ser Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu		
225	230	235	240
	Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly		
	245	250	255
10	Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe		
	260	265	270
	Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg		
	275	280	285
	Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn		
15	290	295	300
	Ser Val Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp		
	305	310	315
	Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met		
	325	330	335
20	Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val		
	340	345	350
	Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr		
	355	360	365
	Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Ile		
25	370	375	380
	Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro		
	385	390	395
	Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe		
	405	410	415
30	Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe		
	420	425	430
	Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp		
	435	440	445
	Arg		
35			

<210> 21

<211> 449

<212> PRT

40 <213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:10

<400> 21

5 Met Asn Tyr Lys Asn Lys Asn Leu Val Ser Glu Ser Gly Leu Thr Gln
1 5 10 15
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln Arg Glu Leu Glu
20 25 30
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
10 35 40 45
Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val
50 55 60
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
65 70 75 80
15 Cys Arg His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala
85 90 95
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ala Asn Gly
100 105 110
Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ala Leu
20 115 120 125
Asp Lys Lys Cys Met Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
130 135 140
His Gly Phe Ile Tyr Gly Cys Phe Asp Glu Glu Ala Pro Ser Leu Lys
145 150 155 160
25 Asp Tyr Met Gly Asp Ala Gly Trp Tyr Leu Glu Pro Met Phe Lys His
165 170 175
Ser Gly Gly Leu Glu Leu Ile Gly Pro Pro Gly Lys Val Ile Ile Lys
180 185 190
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Thr Gly Asp Ala Tyr His
30 195 200 205
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Val Phe
210 215 220
Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
225 230 235 240
35 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
245 250 255
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
260 265 270
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Glu Val Arg
40 275 280 285

Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Phe Leu Thr Cys Ser Gly Val Phe Lys Val Trp His Pro Ile Asp
 305 310 315 320
 5 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Met Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Val Asp Ala Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 10 355 360 365
 Val Ser Gln Asn Ala Lys Lys Tyr Gln Ser Arg Asp Gly Asp Leu Val
 370 375 380
 Ser Asn Leu Gly Phe Gly Gly Asp Val Tyr Gly Asp Glu Val Tyr Pro
 385 390 395 400
 15 Gly Ile Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gly Ala His Ile Ser Ser Ser Ser Trp Ala Glu Phe
 420 425 430
 Glu Asp Val Ser Lys Asn Trp His Thr Glu Leu Ala Lys Thr Thr Asp
 20 435 440 445
 Arg

 <210> 22
 25 <211> 447
 <212> PRT
 <213> Artificial Sequence

 <220>
 30 <223> A polypeptide encoded by SEQ ID NO:11

 <400> 22
 Met Ile Tyr Glu Asn Leu Val Ser Glu Ala Gly Leu Thr Gln Lys His
 1 5 10 15
 35 Leu Ile His Gly Asp Lys Glu Leu Phe Gln His Glu Leu Lys Thr Ile
 20 25 30
 Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser
 35 40 45
 Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val
 40 50 55 60

Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg
 65 70 75 80
 His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala Lys Gly
 85 90 95
 5 Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly Glu Leu
 100 105 110
 Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Thr Ile Lys Lys
 115 120 125
 Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly
 10 130 135 140
 Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Thr Leu Val Asp Tyr
 145 150 155 160
 Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His Ser Gly
 165 170 175
 15 Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys Ala Asn
 180 185 190
 Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His Val Gly
 195 200 205
 Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Ile Phe Thr Pro
 20 210 215 220
 Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly Ala Gly Leu Gln Met
 225 230 235 240
 Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly Tyr Ser
 245 250 255
 25 Gly Val His Ser Ala Asp Leu Val Pro Glu Met Met Ala Phe Gly Gly
 260 265 270
 Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg
 275 280 285
 Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn Ser Ile
 30 290 295 300
 Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp Glu Asn
 305 310 315 320
 Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met Pro Glu
 325 330 335
 35 Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val Gly Pro
 340 345 350
 Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr Glu Ser
 355 360 365
 Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Leu Ile Ala Asn
 40 370 375 380

Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val
 385 390 395 400
 Val Ala Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg
 405 410 415
 5 Ala Tyr Gln Ala His Ile Ser Ser Ser Asn Trp Ala Glu Phe Glu Asn
 420 425 430
 Thr Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg
 435 440 445

10 <210> 23
 <211> 447
 <212> PRT
 <213> Artificial Sequence

15 <220>
 <223> A polypeptide encoded by SEQ ID NO:12

<400> 23

Met Ser Tyr Gln Asn Leu Val Ser Glu Ala Gly Leu Thr Gln Lys Leu
 20 1 5 10 15
 Leu Ile His Gly Asp Lys Glu Leu Phe Gln His Glu Leu Lys Thr Ile
 20 25 30
 Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser
 35 40 45

25 Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val
 50 55 60
 Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg
 65 70 75 80
 His Arg Gly Lys Thr Leu Val His Thr Glu Ala Gly Asn Ala Lys Gly
 80 85 90 95
 Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly Ser Asn Gly Glu Leu
 100 105 110
 Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Ala Ile Lys Lys
 115 120 125

35 Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly
 130 135 140
 Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Pro Leu Ile Asp Tyr
 145 150 155 160
 Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Thr Phe Lys His Ser Gly
 160 165 170 175

Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Val Lys Ala Asn
 180 185 190
 Trp Lys Pro Phe Ala Glu Asn Phe Val Gly Asp Ile Tyr His Val Gly
 195 200 205
 5 Trp Thr His Ala Ala Ala Leu Arg Ala Gly Gln Ser Val Phe Ser Ser
 210 215 220
 Leu Ala Gly Asn Ala Lys Leu Pro Pro Glu Gly Ala Gly Leu Gln Met
 225 230 235 240
 Thr Ser Lys Tyr Gly Ser Gly Met Gly Leu Thr Trp Asp Tyr Tyr Ser
 10 245 250 255
 Gly Asn Phe Ser Ala Asp Met Val Pro Asp Leu Met Ala Phe Gly Ala
 260 265 270
 Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg
 275 280 285
 15 Ile Tyr Arg Ser Ile Leu Asn Gly Thr Val Phe Pro Asn Asn Ser Phe
 290 295 300
 Leu Thr Gly Ser Ala Thr Phe Lys Val Trp Asn Pro Ile Asp Glu Asn
 305 310 315 320
 Thr Thr Glu Val Trp Thr Tyr Ala Phe Val Glu Lys Asp Met Pro Glu
 20 325 330 335
 Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln Arg Ser Val Gly Pro
 340 345 350
 Ala Gly Phe Trp Glu Ser Asp Asp Asn Glu Asn Met Glu Thr Leu Ser
 355 360 365
 25 Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Gln Ile Ala Ser
 370 375 380
 Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val
 385 390 395 400
 Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg
 30 405 410 415
 Ala Tyr Gln Ala His Ile Ser Ser Asn Trp Ala Glu Phe Glu Asn
 420 425 430
 Ala Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg
 435 440 445

35

<210> 24
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<2220>

<2223> A polypeptide encoded by SEQ ID NO:13

<400> 24

5 Met Arg Gln Ala Ile Met Ser Tyr Gln Asn Leu Val Ser Glu Ala Gly
 1 5 10 15
 Leu Thr Gln Lys His Leu Ile Tyr Gly Asp Lys Glu Leu Phe Gln His
 20 25 30
 Glu Leu Lys Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp
 10 35 40 45
 Ser Leu Ile Pro Ser Pro Gly Asp Tyr Val Lys Ala Lys Met Gly Val
 50 55 60
 Asp Glu Val Ile Val Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe
 65 70 75 80
 15 Leu Asn Val Cys Arg His Arg Gly Lys Thr Ile Val Asp Ala Glu Ala
 85 90 95
 Gly Asn Ala Lys Gly Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly
 100 105 110
 Ser Asn Gly Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly
 20 115 120 125
 Asp Ala Ile Lys Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile
 130 135 140
 Glu Ser Phe His Gly Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro
 145 150 155 160
 25 Pro Leu Ile Asp Tyr Leu Gly Asp Val Ala Trp Tyr Leu Glu Pro Thr
 165 170 175
 Phe Lys His Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Ala Lys Val
 180 185 190
 Val Val Lys Gly Asn Trp Lys Val Phe Ala Glu Asn Phe Val Gly Asp
 30 195 200 205
 Ile Tyr His Ile Gly Trp Thr His Ala Ser Ile Leu Arg Ala Gly Gln
 210 215 220
 Ala Ile Phe Ala Pro Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly
 225 230 235 240
 35 Thr Gly Leu Gln Ala Thr Thr Lys Tyr Gly Ser Gly Ile Gly Val Ser
 245 250 255
 Leu Asp Ala Tyr Ser Gly Val Gln Ser Ala Asp Leu Val Pro Glu Met
 260 265 270
 Met Ala Phe Gly Gly Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly
 40 275 280 285

Asp Val Arg Ala Arg Ile Tyr Arg Ser Gln Val Asn Gly Thr Val Phe
 290 295 300
 Pro Asn Asn Cys Phe Leu Thr Gly Ala Gly Val Phe Lys Val Phe Asn
 305 310 315 320
 5 Pro Ile Asp Glu Asn Thr Thr Glu Ala Trp Thr Tyr Ala Ile Val Glu
 325 330 335
 Lys Asp Met Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln
 340 345 350
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 385 390 395 400
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<212> PRT

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Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile

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 5 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
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 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Met Glu Thr
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tgattcagtg	accattttta	caaatggtca	ctgcaaccgc	ggtcaccatt	aatcaaaggg	2220	
aatgtacgtg	tatggcaat	caacaagtcg	tttcgataac	cggtg		2265	
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10							
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	gccctgtcg	cacccgtgac	acagaacatc	aaaacatatc	cagtcaagat	tgagaacctg	120
	cgcgtaatga	ttgatttgag	ctaagaattt	taacaggagg	cacccgggc	cctagagcgt	180
	aatcacccccc	attccatctt	ttttaggtga	aaacatgaat	tacaataata	aaatcttggt	240
	aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gatgaagaac	ttttccaaca	300
20	tgaactgaaa	accatttttgc	cgccgaaactg	gcttttctc	actcatgata	gcctgattcc	360
	tgccccccggc	gactatgtt	ccgcaaaaat	ggggattgac	gaggtcatcg	tctccggca	420
	gaacgacgg	tcgattcgtg	cttttctgaa	cgtttgcgg	catcggtggca	agacgctggt	480
	gagcgtggaa	gccggcaatg	ccaaagggtt	tgtttgcagc	tatcacggct	ggggcttcgg	540
	ctccaacgg	gaactgcaga	gcgttccatt	tgaaaaagat	ctgtacggcg	agtcgctcaa	600
25	taaaaaatgt	ctgggggttga	aagaagtgc	tcgcgtggag	agcttccatg	gcttcatcta	660
	cgggttctc	gaccaggagg	ccctctct	tatggactat	ctgggtgacg	ctgcttggta	720
	cctggAACCT	atgttcaagc	attccggcgg	tttagaactg	gtcggtcctc	caggcaaggt	780
	tgtgtatcaag	gccaactgga	aggcaccgc	ggaaaacttt	gtgggagatg	cataccacgt	840
	gggttggacg	cacgcgtt	cgcttcgctc	gggggagtc	atcttctgt	cgctcgctgg	900
30	caatgcggcg	ctaccacctg	aaggcgcagg	cttgcaaatg	acctccaaat	acggcagcgg	960
	catgggtgt	ttgtggacg	gatattcagg	tgtgcata	gcagacttgg	ttccggaaatt	1020
	gatggcattc	ggaggcgca	agcaggaaag	gctgaacaaa	gaaattggcg	atgttcgcgc	1080
	tcggatttat	cgcagccacc	tcaactgcac	cgtttccc	aacaacagca	tgtgtacactg	1140
	ctcgggtgtt	ttcaaagtat	ggaaccgc	cgacgc	accaccgagg	tctggaccta	1200
35	cgccattgtc	aaaaagaca	tgcctgagga	tctcaagcgc	cgcttggccg	actctgttca	1260
	gcgaacgatc	gggcctgctg	gcttctggga	aagcgacgc	aatgacaata	tggaaacagc	1320
	ttcgc	ggcaagaaat	atcaatcaag	agatagtgt	ctgcttcaa	accttggttt	1380
	cgggtggac	gtatacggcg	acgcggctca	tccagggcgtc	gtcgccaaat	cgcgatcg	1440
	cgagaccagt	tatcgtggtt	tctaccggc	ttaccaggca	cacgtcagca	gttccaactg	1500
40	ggctgagttc	gagcatgcct	ctagtacttg	gcatactgaa	cttacgaaga	ctactgatcg	1560

15 <210> 32
<211> 449
<212> PRT
<213> Artificial Sequence

20 <220>
<223> A polypeptide encoded by SEQ ID NO:27

<400> 32

Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
1 5 10 15

25 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
20 25 30

Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
35 40 45

Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
30 50 55 60

Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
65 70 75 80

Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
85 90 95

35 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
100 105 110

Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
115 120 125

Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
40 130 135 140

His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 5 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 10 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 15 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 20 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 25 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Gly
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 30 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 35 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 33
 <211> 449
 <212> PRT
 <213> Artificial Sequence

5

<220>
 <223> A polypeptide encoded by SEQ ID NO:28

<400> 33

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 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 15 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 20 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 25 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 30 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 35 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 40 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly

	245	250	255
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe			
	260	265	270
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg			
5	275	280	285
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn			
	290	295	300
Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp			
	305	310	315
320			
10	Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met		
	325	330	335
Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ala			
	340	345	350
Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr			
15	355	360	365
Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu			
	370	375	380
Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro			
	385	390	395
400			
20	Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe		
	405	410	415
Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe			
	420	425	430
Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp			
25	435	440	445
Arg			
	<210> 34		
30	<211> 449		
	<212> PRT		
	<213> Artificial Sequence		
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35	<223> A polypeptide encoded by SEQ ID NO:29		
	<400> 34		
Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln			
1	5	10	15
40 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys			

	20	25	30
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile			
35	40	45	
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val			
5 50	55	60	
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val			
65	70	75	80
Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala			
85	90	95	
10 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly			
100	105	110	
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu			
115	120	125	
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe			
15 130	135	140	
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met			
145	150	155	160
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His			
165	170	175	
20 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys			
180	185	190	
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His			
195	200	205	
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe			
25 210	215	220	
Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu			
225	230	235	240
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly			
245	250	255	
30 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe			
260	265	270	
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg			
275	280	285	
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn			
35 290	295	300	
Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp			
305	310	315	320
Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met			
325	330	335	
40 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Thr			

	340	345	350
	Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr		
	355	360	365
	Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu		
5	370	375	380
	Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro		
	385	390	395
	385 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe		
	405	410	415
10	405 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe		
	420	425	430
	420 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp		
	435	440	445
	435 Arg		
15			
	<210> 35		
	<211> 449		
	<212> PRT		
20	<213> Artificial Sequence		
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25	<400> 35		
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	1 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys		
	20	25	30
30	20 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile		
	35	40	45
	35 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val		
	50	55	60
	50 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val		
35	65	70	75
	35 65 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala		
	85	90	95
	85 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly		
	100	105	110
40	100 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu		

115	120	125
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe		
130	135	140
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met		
5 145	150	155
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His		
165	170	175
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys		
180	185	190
10 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His		
195	200	205
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe		
210	215	220
Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu		
15 225	230	235
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly		
245	250	255
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe		
260	265	270
20 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg		
275	280	285
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn		
290	295	300
Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp		
25 305	310	315
Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met		
325	330	335
30 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Leu		
340	345	350
35 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr		
355	360	365
Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu		
370	375	380
35 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro		
385	390	395
Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe		
405	410	415
40 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe		
420	425	430
40 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp		

435

440

445

Arg

5 <210> 36
 <211> 449
 <212> PRT
 <213> Artificial Sequence

10 <220>
 <223> A polypeptide encoded by SEQ ID NO:31

 <400> 36

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 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 20 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 25 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 30 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 35 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 40 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe

210	215	220	
Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu			
225	230	235	240
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly			
5	245	250	255
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe			
260	265	270	
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg			
275	280	285	
10	Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn		
290	295	300	
Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp			
305	310	315	320
Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met			
15	325	330	335
Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ile			
340	345	350	
Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr			
355	360	365	
20	Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu		
370	375	380	
Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro			
385	390	395	400
Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe			
25	405	410	415
Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe			
420	425	430	
Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp			
435	440	445	
30	Arg		

<210> 37
 <211> 22
 35 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> An oligonucleotide

22
 <400> 37
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 5 <210> 38
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 10 <220>
 <223> An oligonucleotide
 <400> 38
 27
 gccgggcctc ttgcggata tcgtcca
 15 <210> 39
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 20 <220>
 <223> An oligonucleotide
 <400> 39
 27
 gttgccattg ctgcaggcat cgtggtg
 25 <210> 40
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 30 <220>
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 <400> 40
 33
 35 gaggcaccccg cggaagctt tgtggagat gca
 <210> 41
 <211> 30
 <212> DNA
 40 <213> Artificial Sequence

<220>
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<400> 41
5 gcacccgcgg aacaatttgt gggagatgca 30

<210> 42
<211> 21
<212> DNA
10 <213> Artificial Sequence

<220>
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15 <400> 42
ccgcggaaag ctttgtggga g 21

<210> 43
<211> 24
20 <212> DNA
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<220>
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25 <400> 43
ccgcggaaaaa gcttgtggga gatg 24

<210> 44
30 <211> 23
<212> DNA
<213> Artificial Sequence

<220>
35 <223> An oligonucleotide

<400> 44
cgcgaaaaac gtttgtggag atg 23

40 <210> 45

5 <220>
 <223> An oligonucleotide

 <400> 45
atattcagg gcgcatacg cag
10 <210> 46
 <211> 34
 <212> DNA
 <213> Artificial Sequence

15 <220>
 <223> An oligonucleotide

 <400> 46
20 ggacggatat tcagggctcc atagcgcaga ctta 23

 <210> 47
 <211> 33
 <212> DNA
25 <213> Artificial Sequence

 <220>
 <223> An oligonucleotide

30 <400> 47
gacggatatt caggtaacca tagcgcagac ttg 33

 <210> 48
 <211> 30
 <212> DNA
35 <213> Artificial Sequence

 <220>
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30

<400> 48
ggtgtttca aagtgcgaa cccgatcgac

5 <210> 49
 <211> 26
 <212> DNA
 <213> Artificial Sequence

10 <220>
 <223> An oligonucleotide

26

<400> 49
ctgttcagcg aaacttcggg cctgct

15 <210> 50
 <211> 26
 <212> DNA
 <213> Artificial Sequence

20 <220>
 <223> An oligonucleotide

26

<400> 50
ctgttcagcg aaggttcggg cctgct

25 <210> 51
 <211> 26
 <212> DNA
 <213> Artificial Sequence

30 <220>
 <223> An oligonucleotide

26

<400> 51
35 ctgttcagcg aagtttcggg cctgct

<210> 52
<211> 22
<212> DNA

40 <213> Artificial Sequence

22

<220>

<223> An oligonucleotide

<400> 52

5 ttcagcgaac gctcgggcct gc

<210> 53

<211> 30

<212> DNA

10 <213> Artificial Sequence

<220>

<223> An oligonucleotide

15 <400> 53

ggcctgctgg cttcgcgaa agcgacgaca

30

<210> 54

<211> 21

<212> DNA

20 <213> Artificial Sequence

<220>

<223> An oligonucleotide

25

<400> 54

gaaagcgacg ccaatgacaa t

21

<210> 55

<211> 30

<212> DNA

30 <213> Artificial Sequence

<220>

<223> An oligonucleotide

35

<400> 55

acgacaatga caattggaa acagcttcgc

30

<210> 56

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<211> 2265
<212> DNA
<213> Artificial Sequence
5      <220>
<223> A modified DNA sequence

      <400> 56

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      cgcgtaatga ttgatttgag ctaagaattt taacaggagg caccggggc cctagagcgt 180
      aatcaccccc attccatctt ttttaggtga aaacatgaat tacaataata aatcttggt 240
      aagtgaatct ggtctgagcc aaaagcacct gattcatggc gatgaagaac tttccaaca 300
      tgaactgaaa accatttttg cgccgaaactg gcttttctc actcatgata gcctgattcc 360
15     tgcccccggc gactatgtta ccgcaaaaat ggggattgac gaggtcatcg tctccggca 420
      gaacgacggt tcgattcgtg cttttctgaa cggttgcgg catcggtggca agacgctgg 480
      gagcgtggaa gcccggcaatg ccaaagggtt tgggtgcgc tatcacggct ggggcttcgg 540
      ctccaacggt gaactgcaga gcgttccatt tgaaaaagat ctgtacggcg agtcgctcaa 600
      taaaaaatgt ctgggggtga aagaagtcgc tcgcgtggag agcttccatg gttcatct 660
20     cggttgccttc gaccaggagg cccctccct tatggactat ctgggtgacg ctgtttggta 720
      cctggaaacct atgttcaagc attccggcg tttagaactg gtcggtcctc caggcaaggt 780
      tgtgtcaag gccaactgga aggcacccgc ggaaaacttt gtgggagatg cataccacgt 840
      gggttggacg caacggttccatt cggttcgtc ggggagatc atcttctcg cgctcgctgg 900
      caatgcggcg ctaccacctg aaggcgcagg cttgcaaatg acctccaaat acggcagcgg 960
25     catgggtgtg ttgtgggacg gatattcagg tgtgcatacg gcagacttgg ttccggaaatt 1020
      gatggcattc ggaggcgaa agcaggaaag gctgaacaaa gaaattggcg atgttcgcgc 1080
      tcggatttat cgcagccacc tcaactgcac cggttcccg aacaacagca tgctgacactg 1140
      ctgggtgtt ttcaaaatgtt ggaacccatg cgacgcacaaac accaccgagg tctggaccta 1200
      cgccattgtc gaaaaagaca tgcctgagga tctcaagcgc cgcttggccg actctgttca 1260
30     cgcgaacgtgg gggcctgctg gcttctggaa aagcgcacgac aatgacaata tggaaacagc 1320
      ttgcgaaaaac ggcaagaaat atcaatcaag agatagtgtat ctgctttcaa accttggttt 1380
      cggtgaggac gtatacggcg acgcggctta tccaggcgac gtcggcaaat cggcgatcgg 1440
      cgagaccagt tatcgtggtt tctaccgggc ttaccaggca cagtcagca gctccaactg 1500
      ggctgagttc gagcatgcct ctagtacttgc gataactgaa cttacgaaga ctactgatcg 1560
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 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
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 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
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 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
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Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
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 25 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
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 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Trp
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 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
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 35 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
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Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
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Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
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Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
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Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
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Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
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Asn Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
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His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
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Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
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